

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/823,746
Source: IPW16
Date Processed by STIC: 4-8-05

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IFW16

RAW SEQUENCE LISTING

DATE: 04/08/2005

PATENT APPLICATION: US/09/823,746

TIME: 11:55:46

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Output Set: N:\CRF4\04062005\I823746.raw

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3 <110> APPLICANT: HANSEN, HANS J.
4      GRIFFITHS, GARY L.
5      MCBRIDE, WILLIAM J.
6      LEUNG, SHUI-ON
7      QU, ZHENGXING
9 <120> TITLE OF INVENTION: PRODUCTION AND USE OF NOVEL PEPTIDE-BASED AGENTS FOR
10     USE WITH BI-SPECIFIC ANTIBODIES
12 <130> FILE REFERENCE: 40923-0074US4
14 <140> CURRENT APPLICATION NUMBER: 09/823,746
15 <141> CURRENT FILING DATE: 2001-04-03
17 <150> PRIOR APPLICATION NUMBER: 09/337,756
18 <151> PRIOR FILING DATE: 1999-06-22
20 <160> NUMBER OF SEQ ID NOS: 18
22 <170> SOFTWARE: PatentIn Ver. 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 339
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
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30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(339)
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34 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic 679 Vb
35     nucleotide sequence
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40   1             5             10             15
42 gag aag gtc act atg acc tgc aaa tcc agt cag agt ctg ttc aac agt      96
43 Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu Phe Asn Ser
44   20             25             30
46 aga acc cga aag aac tac ttg ggt tgg tac cag cag aaa cca ggg cag      144
47 Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln
48   35             40             45
50 tct cct aaa ctt ctg atc tac tgg gca tct act cgg gaa tct ggg gtc      192
51 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
52   50             55             60
54 cct gat cgc ttc aca ggc agt gga tct ggg aca gat ttc act ctc acc      240
55 Pro Asp Arg Phe Thr Gly Ser Gly Thr Asp Phe Thr Leu Thr
56  65             70             75             80
58 atc aac agt gtg cag tct gaa gac ctg gca gtt tat tac tgc act caa      288
59 Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Val Tyr Tyr Cys Thr Gln
60   85             90             95

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62 gtt tat tat ctg tgc acg ttc ggt gct ggg acc aag ctg gag ctg aaa 336
63 Val Tyr Tyr Leu Cys Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
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66 cgg 339
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77     amino acid sequence
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84           20           25           30
86 Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln
87           35           40           45
89 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
90           50           55           60
92 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
93   65           70           75           80
95 Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Val Tyr Tyr Cys Thr Gln
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121 Val Gln Leu Gln Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly Ser
122   1           5           10           15
124 ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc agt att tac acc 96
125 Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr Thr
126           20           25           30
128 atg tct tgg ctt cgc cag act ccg gaa aag agg ctg gag tgg gtc gca 144
129 Met Ser Trp Leu Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala
130           35           40           45
132 acc ctg agt ggt gat ggt gat gac atc tac tat cca gac agt gtg aag 192

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133 Thr Leu Ser Gly Asp Gly Asp Asp Ile Tyr Tyr Pro Asp Ser Val Lys
134      50                      55                      60
136 ggt cga ttc acc atc tcc aga gac aat gcc aag aac aac cta tat ctg      240
137 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr Leu
138 65                      70                      75                      80
140 caa atg aac agt cta agg tct gcg gac acg gcc ttg tat tac tgt gca      288
141 Gln Met Asn Ser Leu Arg Ser Ala Asp Thr Ala Leu Tyr Tyr Cys Ala
142                      85                      90                      95
144 agg gtg cga ctt ggg gac tgg gac ttc gat gtc tgg ggc cca ggg acc      336
145 Arg Val Arg Leu Gly Asp Trp Asp Phe Asp Val Trp Gly Pro Gly Thr
146                      100                      105                      110
148 acg gtc tcc gtc tcc tca                                          354
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150      115
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158 <220> FEATURE:
159 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic 679 Vh
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163 Val Gln Leu Gln Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly Ser
164 1      5      10      15
166 Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr Thr
167      20      25      30
169 Met Ser Trp Leu Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala
170      35      40      45
172 Thr Leu Ser Gly Asp Gly Asp Asp Ile Tyr Tyr Pro Asp Ser Val Lys
173      50      55      60
175 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr Leu
176 65      70      75      80
178 Gln Met Asn Ser Leu Arg Ser Ala Asp Thr Ala Leu Tyr Tyr Cys Ala
179      85      90      95
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194 <220> FEATURE:
195 <221> NAME/KEY: CDS
196 <222> LOCATION: (1)..(741)
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199 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic scFv of
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203 gac att gtg atg tca caa tct cca tcc tcc ctg gct gtg tca cca gga 48
204 Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Pro Gly
205 1 5 10 15
207 gag aag gtc act atg acc tgc aaa tcc agt cag agt ctg ttc aac agt 96
208 Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu Phe Asn Ser
209 20 25 30
211 aga acc cga aag aac tac ttg ggt tgg tac cag cag aaa cca ggg cag 144
212 Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln
213 35 40 45
215 tct cct aaa ctt ctg atc tac tgg gca tct act cgg gaa tct ggg gtc 192
216 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
217 50 55 60
219 cct gat cgc ttc aca ggc agt gga tct ggg aca gat ttc act ctc acc 240
220 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
221 65 70 75 80
223 atc aac agt gtg cag tct gaa gac ctg gca gga ggc tcc gga ggc ggt 288
224 Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Gly Gly Ser Gly Gly Gly
225 85 90 95
227 ggg agt gag gtg cag ctg cag gag tct ggg gga gac tta gtg aag cct 336
228 Gly Ser Glu Val Gln Leu Gln Glu Ser Gly Gly Asp Leu Val Lys Pro
229 100 105 110
231 gga ggg tcc ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc agt 384
232 Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
233 115 120 125
235 att tac acc atg tct tgg ctt cgc cag act ccg gaa aag agg ctg gag 432
236 Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro Glu Lys Arg Leu Glu
237 130 135 140
239 tgg gtc gca acc ctg agt gtt tat tac tgc act caa gtt tat tat ctg 480
240 Trp Val Ala Thr Leu Ser Val Tyr Tyr Cys Thr Gln Val Tyr Tyr Leu
241 145 150 155 160
243 tgc acg ttc ggt gct ggg acc aag ctg gag ctg aaa cga gga ggt ggc 528
244 Cys Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly
245 165 170 175
247 gga tca gga ggc ggt gat ggt gat gac atc tac tat cca gac agt gtg 576
248 Gly Ser Gly Gly Gly Asp Gly Asp Asp Ile Tyr Tyr Pro Asp Ser Val
249 180 185 190
251 aag ggt cga ttc acc atc tcc aga gac aat gcc aag aac aac cta tat 624
252 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr
253 195 200 205
255 ctg caa atg aac agt cta agg tct gcg gac acg gcc ttg tat tac tgt 672
256 Leu Gln Met Asn Ser Leu Arg Ser Ala Asp Thr Ala Leu Tyr Tyr Cys
257 210 215 220
259 gca agg gtg cga ctt ggg gac tgg gac ttc gat gtc tgg ggc caa ggg 720
260 Ala Arg Val Arg Leu Gly Asp Trp Asp Phe Asp Val Trp Gly Gln Gly
261 225 230 235 240
263 acc acg gtc acc gtc tcc tca 741
264 Thr Thr Val Thr Val Ser Ser
265 245
268 <210> SEQ ID NO: 6

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269 <211> LENGTH: 247
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282           20           25           30
284 Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Gln
285           35           40           45
287 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
288           50           55           60
290 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
291   65           70           75           80
293 Ile Asn Ser Val Gln Ser Glu Asp Leu Ala Gly Gly Ser Gly Gly Gly
294           85           90           95
296 Gly Ser Glu Val Gln Leu Gln Glu Ser Gly Gly Asp Leu Val Lys Pro
297           100          105          110
299 Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
300           115          120          125
302 Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro Glu Lys Arg Leu Glu
303   130          135          140
305 Trp Val Ala Thr Leu Ser Val Tyr Tyr Cys Thr Gln Val Tyr Tyr Leu
306 145           150           155           160
308 Cys Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly
309           165           170           175
311 Gly Ser Gly Gly Gly Asp Gly Asp Asp Ile Tyr Tyr Pro Asp Ser Val
312           180           185           190
314 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Asn Leu Tyr
315           195          200          205
317 Leu Gln Met Asn Ser Leu Arg Ser Ala Asp Thr Ala Leu Tyr Tyr Cys
318   210          215          220
320 Ala Arg Val Arg Leu Gly Asp Trp Asp Phe Asp Val Trp Gly Gln Gly
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323 Thr Thr Val Thr Val Ser Ser
324           245
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332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
335 <221> NAME/KEY: CDS
336 <222> LOCATION: (1)..(336)
338 <220> FEATURE:
339 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Mu-9V
340     nucleotide sequence

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VERIFICATION SUMMARY

DATE: 04/08/2005

PATENT APPLICATION: US/09/823,746

TIME: 11:55:47

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